

1718-0195P.ST25.txt

SEQUENCE LISTING

<110> Quibell, Martin
Taylor, Steven
Grabowska, Urszula
Nilsson, Magnus
Morisson, Veronique

<120> Cysteine Protease Inhibitors

<130> 1718-0195P

<150> US 60/252,840

<151> 2000-11-17

<150> PCT/GB00/01894

<151> 2000-05-18

<150> GB9911417.5

<151> 1999-05-18

<160> 4

<170> PatentIn version 3.0

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<212> DNA

<213> artificial sequence

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cgcggtatccg ccacatgga attaacaga ttgcccgat

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<223> Primer for cDNA of cysteinyl proteinase (Falcipain 2)

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<212> DNA

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<223> PCR product from amplification using primers for the cDNA sequence of cysteinyl proteinase (Falcipain 2)

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<221> CDS

<222> (3)..(848)

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1 5 10 15

47

aac aaa tat ctt agt tta aga tct tca aaa cca tta aag aat tct aaa
Asn Lys Tyr Leu Ser Leu Arg Ser Ser Lys Pro Leu Lys Asn Ser Lys
20 25 30

95

tat tta tta gat caa atg aat tat gaa gaa gtt ata aaa aaa tat aga
Tyr Leu Leu Asp Gln Met Asn Tyr Glu Glu Val Ile Lys Lys Tyr Arg
35 40 45

143

gga gaa gaa aat ttc gat cat gca gct tac gac tgg aga tta cac agt
Gly Glu Glu Asn Phe Asp His Ala Ala Tyr Asp Trp Arg Leu His Ser

191

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ggt gta aca cct gta aag gat caa aaa aat tgt gga tct tgc tgg gcc 239
Gly Val Thr Pro Val Lys Asp Gln Lys Asn Cys Gly Ser Cys Trp Ala
  65      70      75

ttt agt agt ata ggt tcc gta gaa tca caa tat gct atc aga aaa aat 287
Phe Ser Ser Ile Gly Ser Val Glu Ser Gln Tyr Ala Ile Arg Lys Asn
  80      85      90      95

aaa tta ata acc tta agt gaa caa gaa tta gta gat tgt tca ttt aaa 335
Lys Leu Ile Thr Leu Ser Glu Gln Glu Val Asp Cys Ser Phe Lys
      100      105      110

aat tat ggt tgt aat gga ggt ctc att aat aat gcc ttt gag gat atg 383
Asn Tyr Gly Cys Asn Gly Gly Leu Ile Asn Asn Ala Phe Glu Asp Met
      115      120      125

att gaa ctt gga ggt ata tgt cca gat ggt gat tat cca tat gtg agt 431
Ile Glu Leu Gly Gly Ile Cys Pro Asp Gly Asp Tyr Pro Tyr Val Ser
      130      135      140

gat gct cca aat tta tgt aac ata gat aga tgt act gaa aaa tat gga 479
Asp Ala Pro Asn Leu Cys Asn Ile Asp Arg Cys Thr Glu Lys Tyr Gly
      145      150      155

atc aaa aat tat tta tcc gta cca gat aat aaa tta aaa gaa gca ctt 527
Ile Lys Asn Tyr Leu Ser Val Pro Asp Asn Lys Leu Lys Glu Ala Leu
      160      165      170      175

aga ttc ttg gga cct att agt att agt gta gcc gta tca gat gat ttt 575
Arg Phe Leu Gly Pro Ile Ser Ile Ser Val Ala Val Ser Asp Asp Phe
      180      185      190

gct ttt tac aaa gaa ggt att ttc gat gga gaa tgt ggt gat gaa tta 623
Ala Phe Tyr Lys Glu Gly Ile Phe Asp Gly Glu Cys Gly Asp Glu Leu
      195      200      205

aat cat gcc gtt atg ctt gta ggt ttt ggt atg aaa gaa att gtt aat 671
Asn His Ala Val Met Leu Val Gly Phe Gly Met Lys Glu Ile Val Asn
      210      215      220

cca tta acc aag aaa gga gaa aaa cat tat tat tat ata att aag aac 719
Pro Leu Thr Lys Lys Gly Glu Lys His Tyr Tyr Tyr Ile Ile Lys Asn
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tca tgg gga caa caa tgg gga gaa aga ggt ttc ata aat att gaa aca 767
Ser Trp Gly Gln Gln Trp Gly Glu Arg Gly Phe Ile Asn Ile Glu Thr
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gat gaa tca gga tta atg aga aaa tgt gga tta ggt act gat gca ttc 815
Asp Glu Ser Gly Leu Met Arg Lys Cys Gly Leu Gly Thr Asp Ala Phe
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att cca tta att gaa cat cat cat cat cat cat taagtcgacg cgatcgaatt 868
Ile Pro Leu Ile Glu His His His His His His
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Leu Leu Asp Gln Met Asn Tyr Glu Glu Val Ile Lys Lys Tyr Arg Gly
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 Glu Glu Asn Phe Asp His Ala Ala Tyr Asp Trp Arg Leu His Ser Gly
 50 55 60
 Val Thr Pro Val Lys Asp Gln Lys Asn Cys Gly Ser Cys Trp Ala Phe
 65 70 75 80
 Ser Ser Ile Gly Ser Val Glu Ser Gln Tyr Ala Ile Arg Lys Asn Lys
 85 90 95
 Leu Ile Thr Leu Ser Glu Gln Glu Leu Val Asp Cys Ser Phe Lys Asn
 100 105 110
 Tyr Gly Cys Asn Gly Gly Leu Ile Asn Asn Ala Phe Glu Asp Met Ile
 115 120 125
 Glu Leu Gly Gly Ile Cys Pro Asp Gly Asp Tyr Pro Tyr Val Ser Asp
 130 135 140
 Ala Pro Asn Leu Cys Asn Ile Asp Arg Cys Thr Glu Lys Tyr Gly Ile
 145 150 155 160
 Lys Asn Tyr Leu Ser Val Pro Asp Asn Lys Leu Lys Glu Ala Leu Arg
 165 170 175
 Phe Leu Gly Pro Ile Ser Ile Ser Val Ala Val Ser Asp Asp Phe Ala
 180 185 190
 Phe Tyr Lys Glu Gly Ile Phe Asp Gly Glu Cys Gly Asp Glu Leu Asn
 195 200 205
 His Ala Val Met Leu Val Gly Phe Gly Met Lys Glu Ile Val Asn Pro
 210 215 220
 Leu Thr Lys Lys Gly Glu Lys His Tyr Tyr Tyr Ile Ile Lys Asn Ser
 225 230 235 240
 Trp Gly Gln Gln Trp Gly Glu Arg Gly Phe Ile Asn Ile Glu Thr Asp
 245 250 255
 Glu Ser Gly Leu Met Arg Lys Cys Gly Leu Gly Thr Asp Ala Phe Ile
 260 265 270
 Pro Leu Ile Glu His His His His His His
 275 280